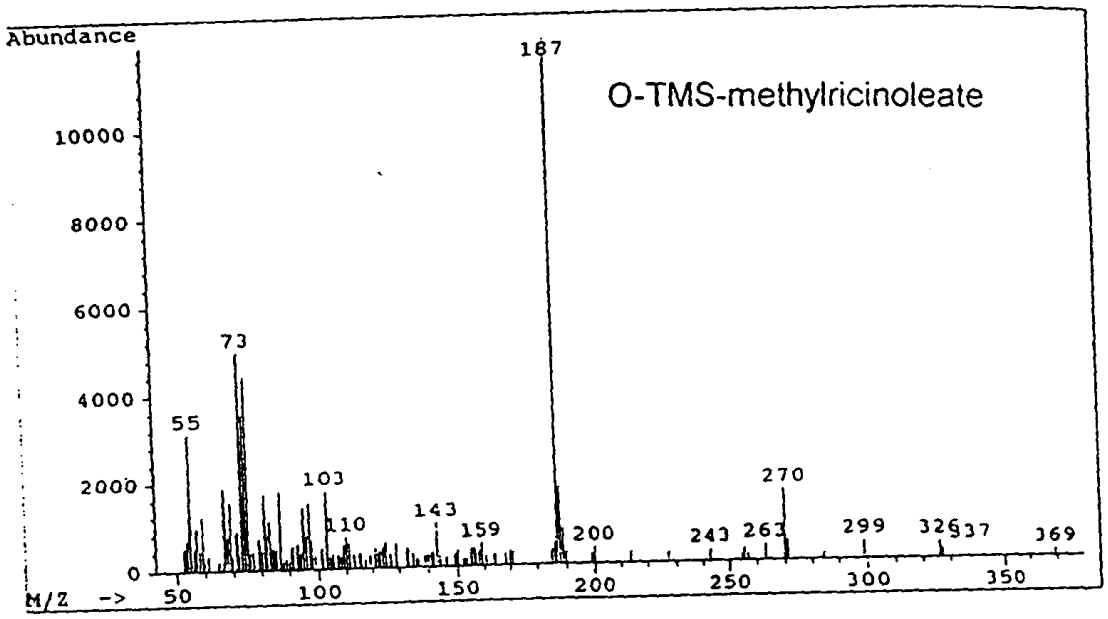
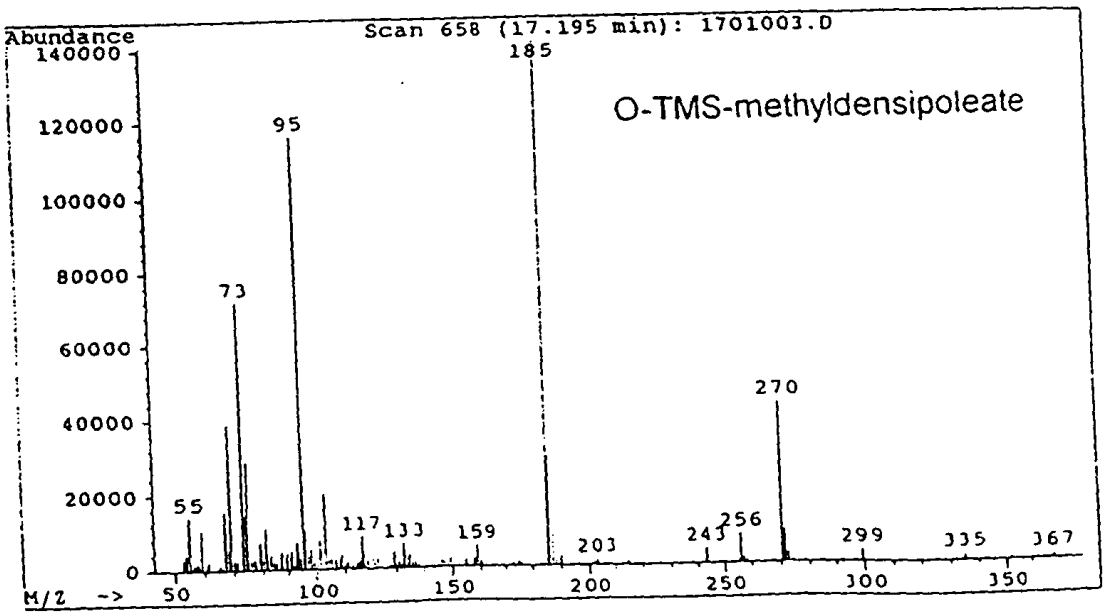
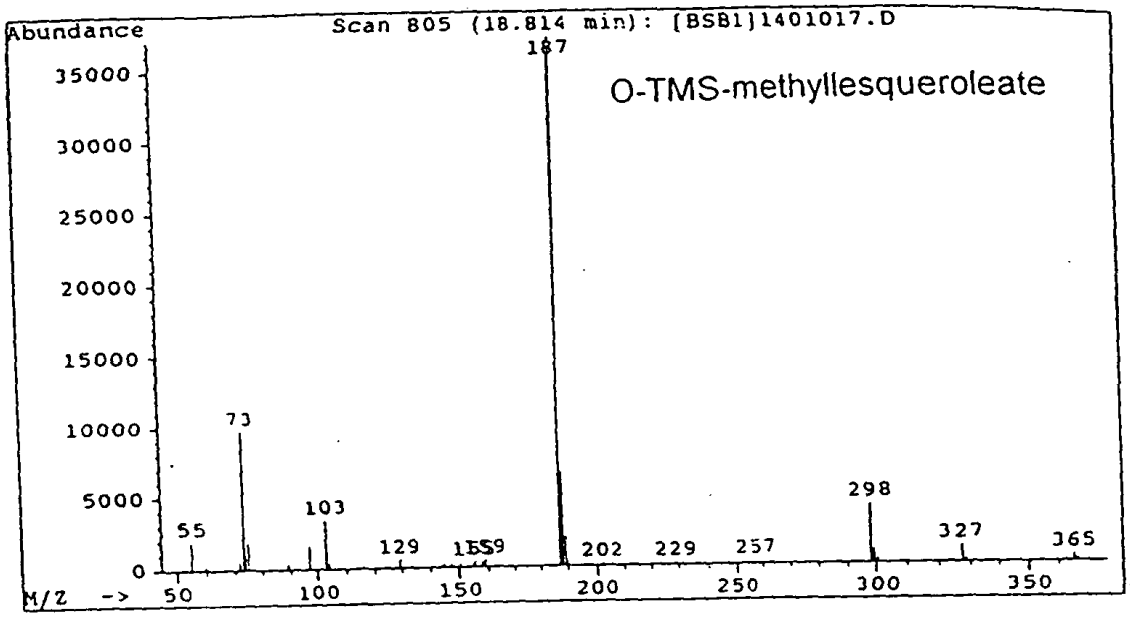
Figure 1A


Abundance
187
O-TMS-methylricinoleate
10000
8000
6000
4000
2000
0
73
55
103
110
143
159
200
243
263
270
299
326
337
369
M/Z ->
50
100
150
200
250
300
350

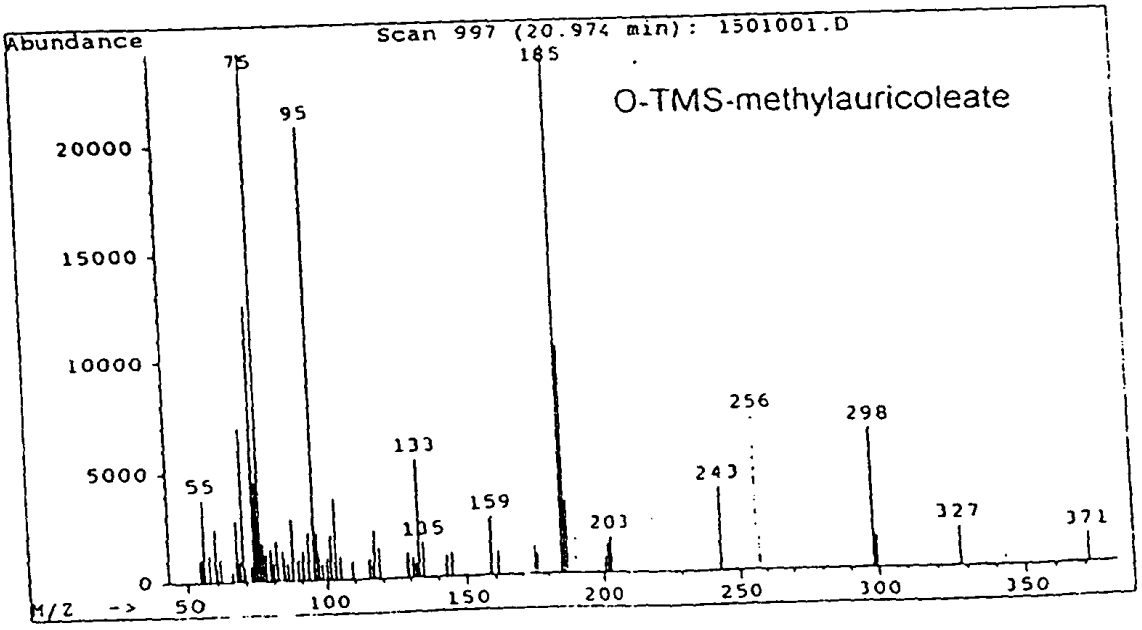
1B

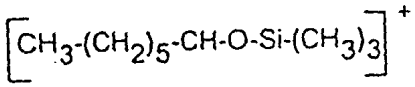

Abundance
Scan 658 (17.195 min): 1701003.D
185
O-TMS-methyldensipoleate
140000
120000
100000
80000
60000
40000
20000
0
95
73
55
117
133
159
203
243
256
270
299
335
367
M/Z ->
50
100
150
200
250
300
350

1C

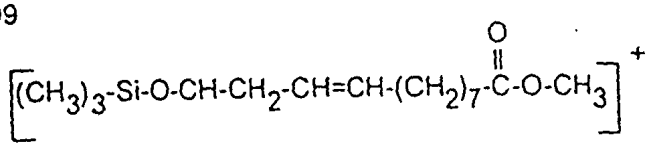

Abundance
Scan 805 (18.814 min): [BSB1]1401017.D
O-TMS-methyllesqueroleate
35000
30000
25000
20000
15000
10000
5000
0
M/Z ->
50
100
150
200
250
300
350
73
103
129
187
202
229
257
298
327
365

1D

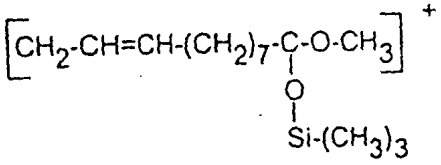

Abundance
Scan 997 (20.974 min): 1501001.D
O-TMS-methylauricoleate
20000
15000
10000
5000
0
M/Z ->
50
100
150
200
250
300
350
75
95
185
55
133
159
105
203
243
256
298
327
371

Ion #1: Mass 187 

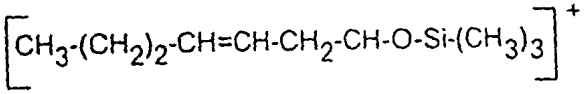
Ion #2: Mass 299



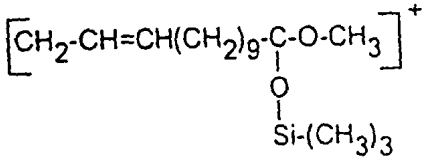
Ion #3: Mass 270 (characteristic rearrangement ion)



Ion #4: Mass 185 (desaturated analog of Ion #1)



Ion #5: Mass 298 (elongated analog of Ion #3)



Ion #6: Mass 327 (elongated analog of ion

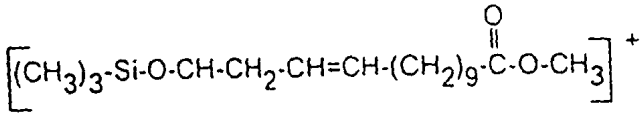


Figure 2

Figure 3

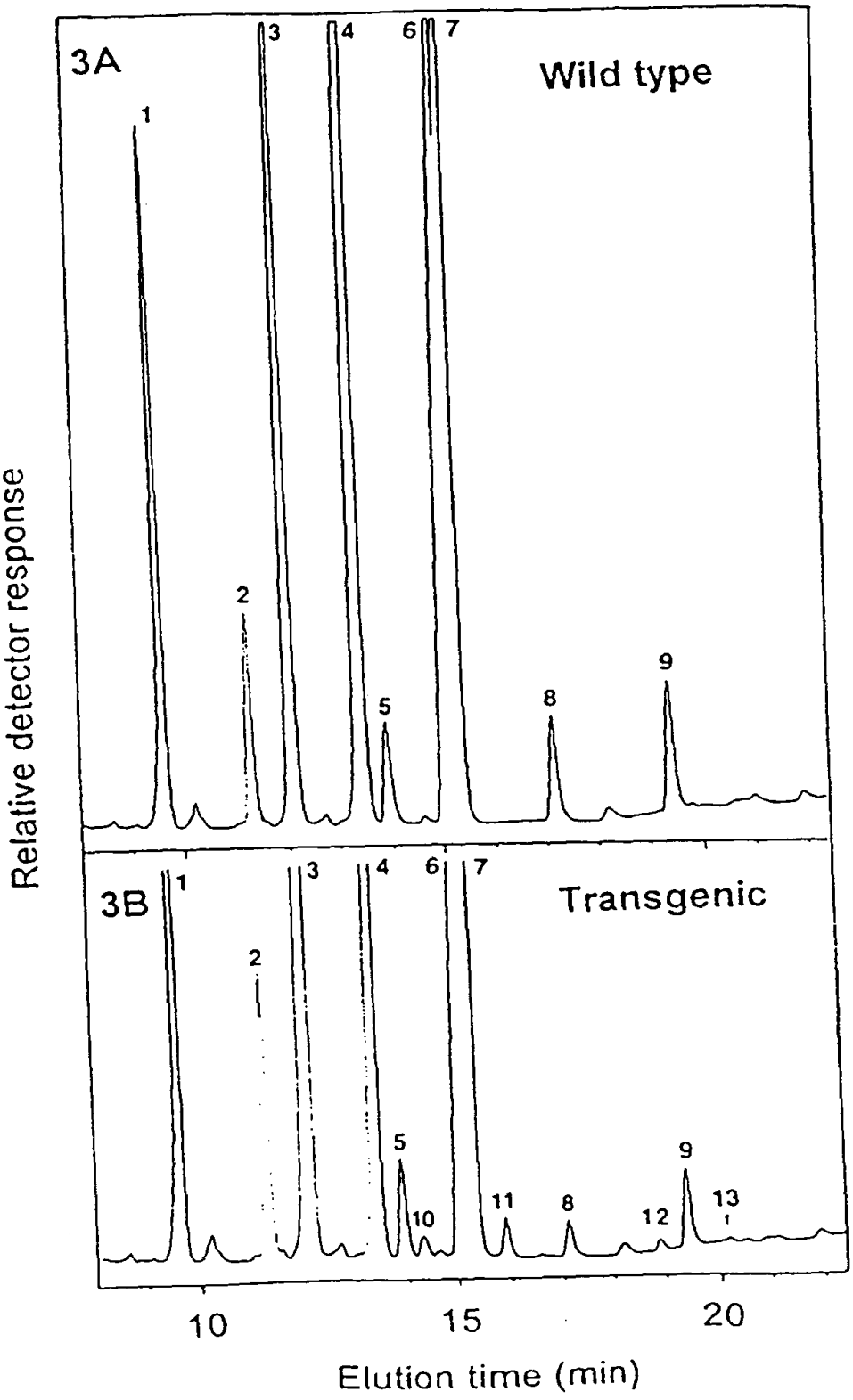
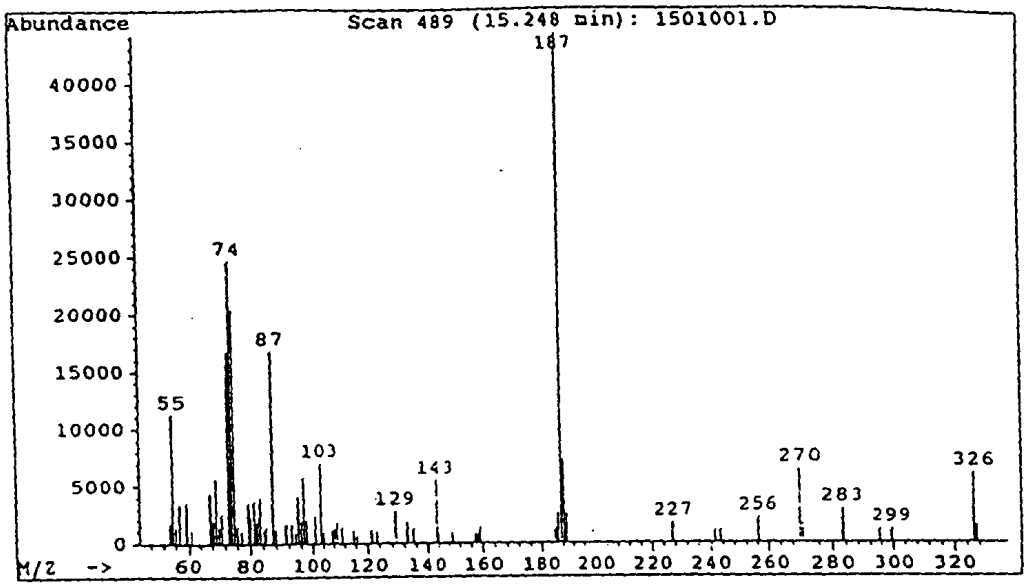
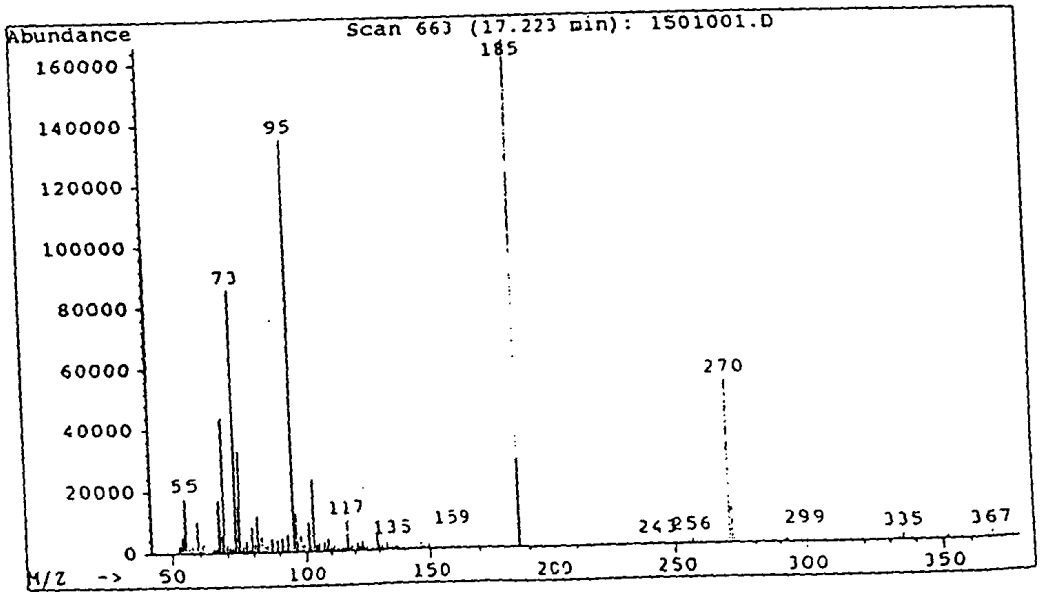

3A
Wild type
1
2
3
4
5
6
7
8
9
3B
Transgenic
1
2
3
4
5
6
7
8
9
10
11
12
13
Relative detector response
10
15
20
Elution time (min)

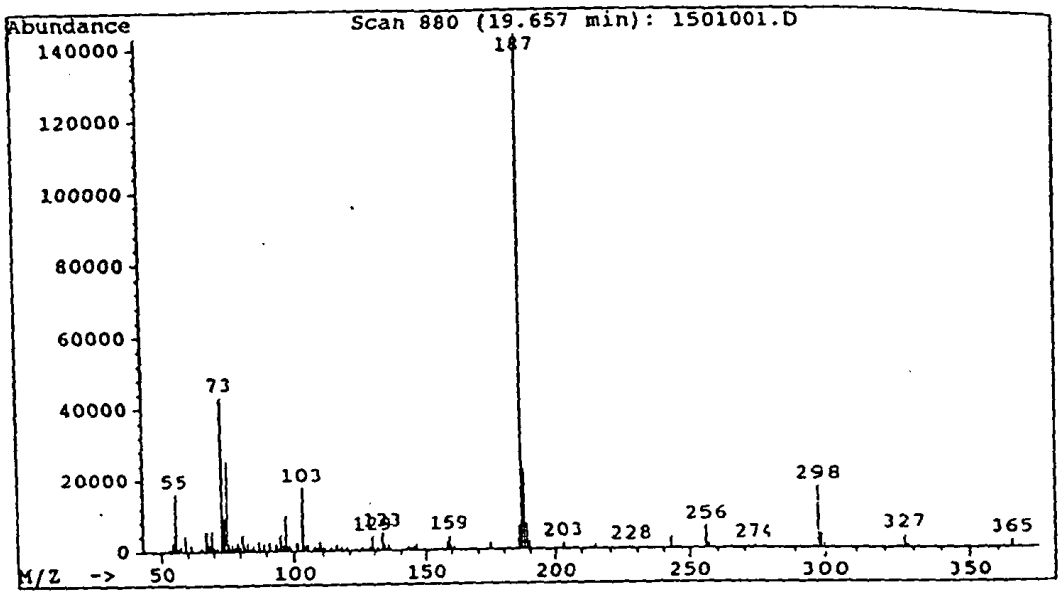
Figure 4A Mass spectrum of peak 10 from figure 3B



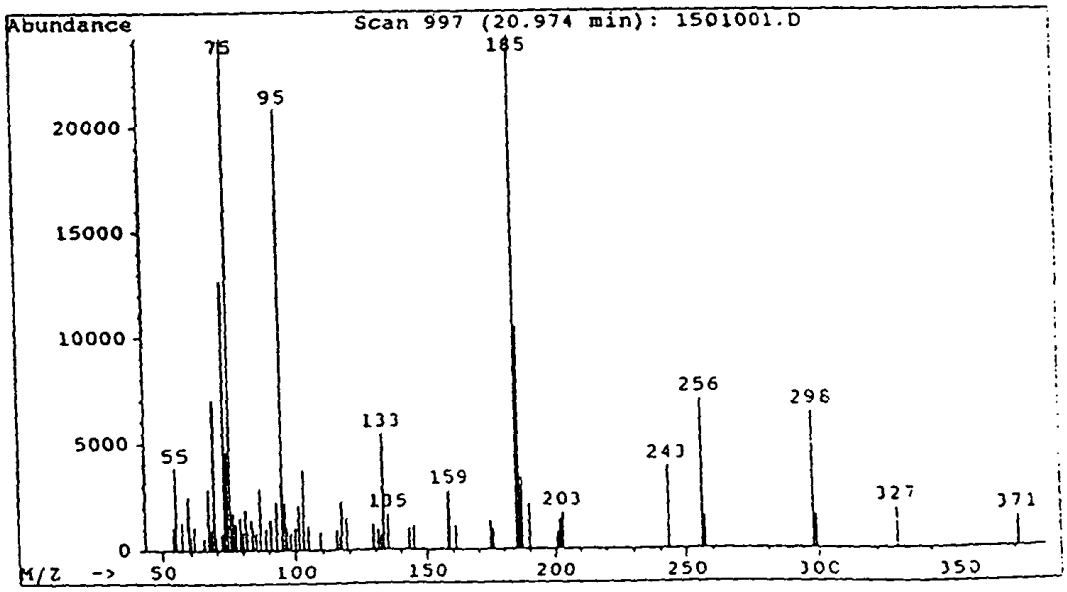
4B Mass spectrum of peak 11 from figure 3B



4C Mass spectrum of peak 12 from figure 3B



4D Mass spectrum of peak 13 from figure 3B



```
        10          20          30          40          50          60
TATTGGCACC  GGCGGCACCA  TTCCAACAAT  GGATCCCTAG  AAAAAGATGA  AGTCTTTGTC
        70          80          90         100         110         120
CCACCTAAGA  AAGCTGCAGT  CANATGGTAT  GTCAAATACC  TCAACAACCC  TCTTGGACGC
       130         140         150         160         170         180
ATTCTGGTGT  TAACAGTTCA  GTTTATCCTC  GGGTGGCCTT  TGTATCTAGC  CTTTAATGTA
       190         200         210         220         230         240
TCAGGTAGAC  CTTATGATGG  TTTCGCTTCA  CATTTCTTCC  CTCATGCACC  TATCTTTAAG
       250         260         270         280         290         300
GACCGTGAAC  GTCTCCAGAT  ATACATCTCA  GATGCTGGTA  TTCTAGCTGT  CTGTTATGGT
       310         320         330         340         350         360
CTTTACCGTT  ACGCTGCTTC  ACAAGGATTG  ACTGCTATGA  TCTGCGTCTA  CGGAGTACCG
       370         380         390         400         410         420
CTTTTGATAG  TGAACTTTTT  CCTTGTCTTG  GTCACTTTCT  TGCAGCACAC  TCATCCTTCA
       430         440         450         460         470         480
TTACCTCACT  ATGATTCAAC  CGAGTGGGAA  TGGATTAGAG  GAGCTTTGGT  TACGGTAGAC
       490         500         510         520         530         540
AGAGACTATG  GAATCTTGAA  CAAGGTGTTT  CACAACATAA  CAGACACCCA  CGTAGCACAC
       550
CAC
```

Figure 5

```
        10          20          30          40          50          60
TATAGGCACC  GGAGGCACCA  TTCCAACACA  GGATCCCTCG  AAAGAGATGA  AGTATTTGTC
        70          80          90         100         110         120
CCAAAGCAGA  AATCCGCAAT  CAAGTGGTAC  GGCGAATACC  TCAACAACCC  TCCTGGTCGC
       130         140         150         160         170         180
ATCATGATGT  TAACTGTCCA  GTTCGTCCTC  GGATGGCCCT  TGTACTTAGC  CTTCAACGTT
       190         200         210         220         230         240
TCTGGCAGAC  CCTACAATGG  TTTCGCTTCC  CATTTCTTCC  CCAATGCTCC  TATCTACAAC
       250         260         270         280         290         300
GACCGTGAAC  GCCTCCAGAT  TTACATCTCT  GATGCTGGTA  TTCTAGCCGT  CTGTTATGGT
       310         320         330         340         350         360
CTTTACCGTT  ACGCTGTTGC  ACAAGGACTA  GCCTCAATGA  TCTGTCTAAA  CGGAGTTCCG
       370         380         390         400         410         420
CTTCTGATAG  TTAACTTTTT  CCTCGTCTTG  ATCACTTACT  TACAACACAC  TCACCCTGCG
       430         440         450         460         470         480
TTGCCTCACT  ATGATTCATC  AGAGTGGGAT  TGGCTTAGAG  GAGCTTTAGC  TACTGTAGAC
       490         500         510         520         530         540
AGAGACTATG  GAATCTTGAA  CAAGGTGTTC  CATAACATCA  CAGACACCCA  CGTCGCACAC
       550
CACT
```

Figure 6

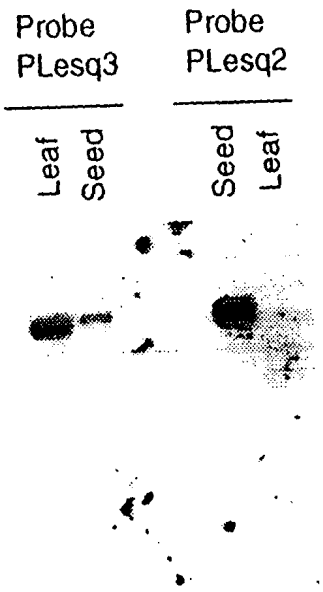


FIG.7

```
AT GAA GCT TTA TAA GAA ETT AGT TTT CTC TGG TGA CAG AGA AAT TNT      47

GTC AAT TGG TAG TGA CAG TTG AAG CAA CAG GAA CAA CAA GGA TGG TTG     95

GTG NTG ATG CTG ATG TGG TGA TGT GTT ATT CAT CAA ATA CTA AAT ACT    143

ACA TTA CTT GTT GCT GCC TAC TTC TCC TAT TTC CTC CGC CAC CCA TTT    191

TGG ACC CAC GAN CCT TCC ATT TAA ACC CTC TCT CGT GCT ATT CAC CAG    239

AAG AGA AGC CAA GAG AGA GAG AGA GAG AAT GTT CTG AGG ATC ATT GTC    287

TTC TTC ATC GTT ATT AAC GTA AGT TTT TTT TGA CCA CTC ATA TCT AAA    335

ATC TAG TAC ATG CAA TAG ATT AAT GAC TGT TCC TTC TTT TGA TAT TTT    383

                        Met Gly Ala Gly Gly Arg Ile Met Val Thr     10
CAG CTT CTT GAA TTC AAG ATG GGT GCT GGT GGA AGA ATA ATG GTT ACC    431

Pro Ser Ser Lys Lys Ser Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys     26
CCC TCT TCC AAG AAA TCA GAA ACT GAA GCC CTA AAA CGT GGA CCA TGT    479

Glu Lys Pro Pro Phe Thr Val Lys Asp Leu Lys Lys Ala Ile Pro Gln     42
GAG AAA CCA CCA TTC ACT GTT AAA GAT CTG AAG AAA GCA ATC CCA CAG    527

His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr     58
CAT TGT TTC AAG CGC TCT ATC CCT CGT TCT TTC TCC TAC CTT CTC ACA    575

Asp Ile Thr Leu Val Ser Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe     74
GAT ATC ACT TTA GTT TCT TGC TTC TAC TAC GTT GCC ACA AAT TAC TTC    623

Ser Leu Leu Pro Gln Pro Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr     90
TCT CTT CTT CCT CAG CCT CTC TCT ACT TAC CTA GCT TGG CCT CTC TAT    671

Trp Val Cys Gln Gly Cys Val Leu Thr Gly Ile Trp Val Ile Gly His    106
TGG GTA TGT CAA GGC TGT GTC TTA ACC GGT ATC TGG GTC ATT GGC CAT    719

Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr    122
GAA TGT GGT CAC CAT GCA TTC AGT GAC TAT CAA TGG GTA GAT GAC ACT    767

Val Gly Phe Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp    138
GTT GGT TTT ATC TTC CAT TCC TTC CTT CTC GTC CCT TAC TTC TCC TGG    815

Lys Tyr Ser His Arg Arg His His Ser Asn Asn Gly Ser Leu Glu Lys    154
AAA TAC AGT CAT CGT CGT CAC CAT TCC AAC AAT GGA TCT CTC GAG AAA    863

Asp Glu Val Phe Val Pro Pro Lys Lys Ala Ala Val Lys Trp Tyr Val    170
GAT GAA GTC TTT GTC CCA CCG AAG AAA GCT GCA GTC AAA TGG TAT GTT    911

Lys Tyr Leu Asn Asn Pro Leu Gly Arg Ile Leu Val Leu Thr Val Gln    186
AAA TAC CTC AAC AAC CCT CTT GGA CGC ATT CTG GTG TTA ACA GTT CAG    959
```

Figure 8A

```
Phe Ile Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg      202
TTT ATC CTC GGG TGG CCT TTG TAT CTA GCC TTT AAT GTA TCA GGT AGA     1007

Pro Tyr Asp Gly Phe Ala Ser His Phe Phe Pro His Ala Pro Ile Phe      218
CCT TAT GAT GGT TTC GCT TCA CAT TTC TTC CCT CAT GCA CCT ATC TTT     1055

Lys Asp Arg Glu Arg Leu Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu      234
AAA GAC CGA GAA CGC CTC CAG ATA TAC ATC TCA GAT GCT GGT ATT CTA     1103

Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr      250
GCT GTC TGT TAT GGT CTT TAC CGT TAC GCT GCT TCA CAA GGA TTG ACT     1151

Ala Met Ile Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Phe Phe      266
GCT ATG ATC TGC GTC TAT GGA GTA CCG CTT TTG ATA GTG AAC TTT TTC     1199

Leu Val Leu Val Thr Phe Leu Gln His Thr His Pro Ser Leu Pro His      282
CTT GTC TTG GTA ACT TTC TTG CAG CAC ACT CAT CCT TCG TTA CCT CAT     1247

Tyr Asp Ser Thr Glu Trp Glu Trp Ile Arg Gly Ala Leu Val Thr Val      298
TAT GAT TCA ACC GAG TGG GAA TGG ATT AGA GGA GCT TTG GTT ACG GTA     1295

Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp      314
GAC AGA GAC TAT GGA ATA TTG AAC AAG GTG TTC CAT AAC ATA ACA GAC     1343

Thr His Val Ala His His Leu Phe Ala Thr Ile Pro His Tyr Asn Ala      330
ACA CAT GTG GCT CAT CAT CTC TTT GCA ACT ATA CCG CAT TAT AAC GCA     1391

Met Glu Ala Thr Glu Ala Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His      346
ATG GAA GCT ACA GAG GCG ATA AAG CCA ATA CTT GGT GAT TAC TAC CAC     1439

Phe Asp Gly Thr Pro Trp Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu      362
TTC GAT GGA ACA CCG TGG TAT GTG GCC ATG TAT AGG GAA GCA AAG GAG     1487

Cys Leu Tyr Val Glu Pro Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr      378
TGT CTC TAT GTA GAA CCG GAT ACG GAA CGT GGG AAG AAA GGT GTC TAC     1535

Tyr Tyr Asn Asn Lys Leu                                             384
TAT TAC AAC AAT AAG TTA TGA GGC TGA TAG GGC GAG AGA AGT GCA ATT     1583

ATC AAT CTT CAT TTC CAT GTT TTA GGT GTC TTG TTT AAG AAG CTA TGC     1631

TTT GTT TCA ATA ATC TCA GAG TCC ATN TAG TTG TGT TCT GGT GCA TTT     1679

TGC CTA GTT ATG TGG TGT CGG AAG TTA GTG TTC AAA CTG CTT CCT GCT     1727

GTG CTG CCC AGT GAA GAA CAA GTT TAC GTG TTT AAA ATA CTC GGA ACG     1775

AAT TGA CCA CAA NAT ATC CAA AAC CGG CTA TCC GAA TTC CAT ATC CGA     1823

AAA CCG GAT ATC CAA ATT TCC AGA GTA CTT AG                          1855
```

Figure 8B

```
                    10         20         30         40         50
LFFAH12     1 MGAGGRIM-- --VTPSSKKS --ETEALKRG PCEKPPFTVK DLKKAIPQHC      50
FAH12       1 MGGGGRMSTV ITSNNSEKKG --GSSHLKRA PHTKPPFTLG DLKRAIPPHC      50
ATFAD2      1 MGAGGRMP-- --VPTSSKKS --ETDTTKRV PCEKPPFSVG DLKKAIPPHC      50
BNFAD2      1 MGAGGRMQ-- --VSPPSKKS --ETDNIKRV PCETPPFTVG ELKKAIPPHC      50
GMFAD2-1    1 MGLA-KETTM GGRGRVAKVE VQGKKPLSRV PNTKPPFTVG QLKKAIPPHC      50
GMFAD2-2    1 MGAGGR---- TDVPPANRKS --EVDPLKRV PFEKPQFSLS QIKKAIPPHC      50
ZMFAD2      1 MGAGGRMTEK EREKQEQLAR ATGGAAMQRS PVEKPPFTLG QIKKAIPPHC      50
RCFAD2      1 ---------- ---------- ---------- ---------- ----------      50
                    60         70         80         90        100
LFFAH12    51 FKRSIPRSFS YLLTDITLVS CFYYVATNYF SLLPQPLSTY LAWPLYWVCQ     100
FAH12      51 FERSFVRSFS YVAYDVCLSF LFYSIATNFF PYISSPLS-Y VAWLVYWLFQ     100
ATFAD2     51 FKRSIPRSFS YLISDIIIAS CFYYVATNYF SLLPQPLS-Y LAWPLYWACQ     100
BNFAD2     51 FKRSIPRSFS HLIWDIIIAS CFYYVATTYF PLLPNPLS-Y FAWPLYWACQ     100
GMFAD2-1   51 FQRSLLTSFS YVVYDLSFAF IFY-IATTYF HLLPQPFS-L IAWPIYWVLQ     100
GMFAD2-2   51 FQRSVLRSFS YVVYDLTIAF CLYYVATHYF HLLPGPLS-F RGMAIYWAVQ     100
ZMFAD2     51 FERSVLKSFS YVVHDLVIAA ALLYFALAII PALPSPLR-Y AAWPLYWIAQ     100
RCFAD2     51 ---------- ---------- ---------- ---------- ----------     100
                   110        120        130        140        150
LFFAH12   101 GCVLTGIWVI GHECGHHAFS DYQWVDDTVG FIFHSFLLVP YFSWKYSHRR     150
FAH12     101 GCILTGLWVI GHECGHHAFS EYQLADDIVG LIVHSALLVP YFSWKYSHRR     150
ATFAD2    101 GCVLTGIWVI AHECGHHAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR     150
BNFAD2    101 GCVLTGVWVI AHECGHAAFS DYQWLDDTVG LIFHSFLLVP YFSWKYSHRR     150
GMFAD2-1  101 GCLLTGVWVI AHECGHHAFS KYQWVDDVVG LTLHSTLLVP YFSWKISHRR     150
GMFAD2-2  101 GCILTGVWVI AHECGHHAFS DYQLLDDIVG LILHSALLVP YFSWKYSHRR     150
ZMFAD2    101 G--------- -------AFS DYSLLDDVVG LVLHSSLMVP YFSWKYSHRR     150
RCFAD2    101 -------WVM AHDCGHHAFS DYQLLDDVVG LILHSCLLVP YFSWKHSHRR     150
                   160        170        180        190        200
LFFAH12   151 HHSNNGSLEK DEVFVPPKKA AVKWYVKYL- NNPLGRILVL TVQFILGWPL     200
FAH12     151 HHSNIGSLER DEVFVPKSKS KISWYSKYS- NNPPGRVLTL AATLLLGWPL     200
ATFAD2    151 HHSNTGSLER DEVFVPKQKS AIKWYGKYL- NNPLGRIMML TVQFVLGWPL     200
BNFAD2    151 HHSNTGSLER DEVFVPR-RS QTSSGTAST- STTFGRTVML TVQFTLGWPL     200
GMFAD2-1  151 HHSNTGSLDR DEVFVPKPKS KVAWFSKYL- NNPLGRAVSL LVTLTIGWPM     200
GMFAD2-2  151 HHSNTGSLER DEVFVPKQKS CIKWYSKYL- NNPPGRVLTL AVTLTLGWPL     200
ZMFAD2    151 HHSNTGSLER DEVFVPKKKE ALPWYTPYVY NNPVGRVVHI VVQLTLGWPL     200
RCFAD2    151 HHSNTGSLER DEVFVPKKKS SIRWYSKYL- NNPPGRIMTI AVTLSLGWPL     200
                   210        220        230        240        250
LFFAH12   201 YLAFNVSGRP YDG-FASHFF PHAPIFKDRE RLQIYISDAG ILAVCYGLYR     250
FAH12     201 YLAFNVSGRP YDR-FACHYD PYGPIFSERE RLQIYIADLG IFATTFVLYQ     250
ATFAD2    201 YLAFNVSGRP YDG-FACHFF PNAPIYNDRE RLQIYLSDAG ILAVCFGLYR     250
BNFAD2    201 YLAFNVSGRP YDGGFACHFH PNAPIYNDRE RLQIYISDAG ILAVCYGLLP     250
GMFAD2-1  201 YLAFNVSGRP YDS-FASHYH PYAPIYSNRE RLLIYVSDVA LFSVTYSLYR     250
GMFAD2-2  201 YLALNVSGRP YDR-FACHYD PYGPIYSDRE RLQIYISDAG VLAVVYGLFR     250
ZMFAD2    201 YLATNASGRP YPR-FACHFD PYGPIYNDRE RAQIFVSDAG VVAVAFGLYK     250
RCFAD2    201 YLAFNVSGRP YDR-FACHYD PYGPIYNDRE RIEIFISDAG VLAVTFGLYQ     250
```

Figure 9A

```
                      260        270        280        290        300
LFFAH12   251 YAASQGLTAM ICVYGVPLLI VNFFLVLVTF LQHTHPSLPH YDSTEWEWIR   300
FAH12     251 ATMAKGLAWV MRIYGVPLLI VNCFLVHITY LQHTHPAIPR YGSSEWDWLR   300
ATFAD2    251 YAAAQGMASM ICLYGVPLLI VNAFLVLITY LQHTHPSLPH YDSSEWDWLR   300
BNFAD2    251 YAAVQGVASM VCFLRVPLLI VNGFLVLITY LQHTHPSLPH YDSSEWDWLR   300
GMFAD2-1  251 VATLKGLVWL LCVYGVPLLI VNGFLVTITY LQHTHFALPH YDSSEWDWLK   300
GMFAD2-2  251 LAMAKGLAWV VCVYGVPLLV VNGFLVLITF LQHTHPALPH YTSSEWDWLR   300
ZMFAD2    251 LAAAFGVWWV VRVYAVPLLI VNAWLVLITY LQHTHPSLPH YDSSEWDWLR   300
RCFAD2    251 LAIAKGLAWV VCVYGVPLLV VNSFLVLITF LQHTHPALPH YDSSEWDWLR   300

                      310        320        330        340        350
LFFAH12   301 GALVTVDRDY GILNKVFHNI TDTHVAHHLF ATIPHYNAME ATEAIKPILG   350
FAH12     301 GAMVTVDRDY GVLNKVFHNI ADTHVAHHLF ATVPHYHAME ATKAIKPIMG   350
ATFAD2    301 GALATVDRDY GILNKVFHNI TDTHVAHHLF STMPHYNAME ATKAIKPILG   350
BNFAD2    301 GALATVDRDY GILNQGFHNI TDTHEAHHLF STMPHYHAME ATKAIKPILG   350
GMFAD2-1  301 GALATMDRDY GILNKVFHHI TDTHVAHHLF STMPHYHAME ATNAIKPILG   350
GMFAD2-2  301 GALATVDRDY GILNKVFHNI TDTHVAHHLF STMPHYHAME ATKAIKPILG   350
ZMFAD2    301 GALATMDRDY GILNRVFHNI TDTHVAHHLF STMPHYHAME ATKAIRPILG   350
RCFAD2    301 GALATVDRDY GILNKVFHNI TDTQVAHHLF ---------- ----------   350
                      360        370        380        390        400
LFFAH12   351 DYYHFDGTPW YVAMYREAKE CLYVEPDTER GKKGVYYYNN K-L.......   400
FAH12     351 EYYRYDGTPF YKALWREAKE CLFVEPDEGA PTQGVFWYRN KY-.......   400
ATFAD2    351 DYYQFDGTPW YVAMYREAKE CIYVEPDREG DKKGVYWYNN K-L.......   400
BNFAD2    351 EYYQFDGTPV VKAMWREAKE CIYVEPDRQG EKKGVFWYNN KL*.......   400
GMFAD2-1  351 EYYQFDDTPF YKALWREARE CLYVEPDEGT SEKGVYWYRN KY-.......   400
GMFAD2-2  351 EYYRFDETPF VKAMWREARE CIYVEPDQST ESKGVFWYNN KL-.......   400
ZMFAD2    351 DYYHFDPTPV AKATWREAGE CIYVEPE--- DRKGVFWYNK KF*.......   400
```

Figure 9B

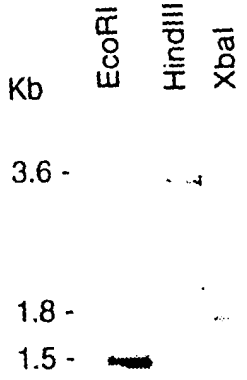
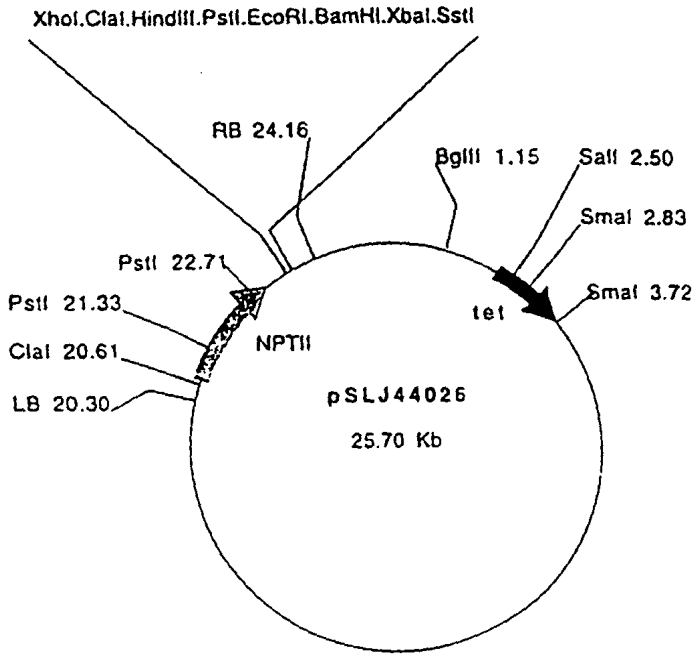


FIG.10



Plasmid name: pSLJ44026
Plasmid size: 25.70 kb
Constructed by: Jonathon Jones
Construction date: 1992
Comments/References: Transgenic Research 1,285-297 (1992)

Figure 11